



# SEQUENCE LISTING

<110> SCHLEHUBER, STEFFEN  
<120> MUTEINS OF THE BILIN-BINDING PROTEIN  
<130> 029029/0101  
<140> 09/980,862  
<141> 2001-12-07  
<150> DE 199 26 068.0  
<151> 1999-06-08  
<160> 27  
<170> PatentIn Ver. 2.1  
<210> 1  
<211> 1219  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: pBBP20  
nucleic acid sequence  
<220>  
<221> sig\_peptide  
<222> (22)..(84)  
<220>  
<221> mat\_peptide  
<222> (85)..(1209)  
<223> fusion protein of bilin-binding protein, Strep-tag II  
and fragment of phage coat protein pIII  
<220>  
<221> CDS  
<222> (85)..(606)  
<223> mature bilin-binding protein  
<220>  
<221> CDS  
<222> (607)..(636)  
<223> Strep-tag II-affinity tag  
<220>  
<221> misc\_feature  
<222> (637)..(639)  
<223> amber stop codon  
<220>  
<221> CDS  
<222> (640)..(1209)  
<223> amino acids 217-406 of coat protein pIII

<400> 1

tctagttaac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg  
51

Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
-20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac  
99

Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp  
-10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag  
147

Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln  
10 15 20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag  
195

Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu  
25 30 35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt  
243

Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser  
40 45 50

gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att  
291

Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile  
55 60 65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac  
339

Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr  
70 75 80 85

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta  
387

His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val  
90 95 100

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac  
435

Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr  
105 110 115

gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga  
483

Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg  
120 125 130

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt  
531

Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu  
135 140 145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc  
 579  
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
 150 155 160 165

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag  
 627  
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln  
 170 175 180

ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc  
 675  
 Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 185 190 195

tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct  
 723  
 Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser  
 200 205 210

gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat  
 771  
 Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr  
 215 220 225

gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat  
 819  
 Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp  
 230 235 240 245

gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct  
 867  
 Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala  
 250 255 260

act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc  
 915  
 Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly  
 265 270 275

ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc  
 963  
 Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser  
 280 285 290

caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat  
 1011  
 Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn  
 295 300 305

ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct  
 1059  
 Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro  
 310 315 320 325

ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac  
 1107

Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp  
330 335 340

aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc  
1155

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala  
345 350 355

acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag  
1203

Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys  
360 365 370

gag tct taataagctt  
1219

Glu Ser  
375

<210> 2

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified\_base

<222> (35)..(36)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (38)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (41)..(42)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (44)..(45)

<223> a, t, c, g, other or unknown

<400> 2

ccatggtaaa tgggtgggaag tcgccaaata ccccnknms nnsnnkaagt acggaaagtg  
60

cgga

64

<210> 3

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified\_base

<222> (19)..(20)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (46)..(47)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (52)..(53)

<223> a, t, c, g, other or unknown

<400> 3

gggtaggcgg taccttcnn aaagtattcc ttgccgtgga ttacmngta snnogaaact

60

ttgacactct t

71

<210> 4

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified\_base

<222> (27)..(28)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (33)..(34)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (42)..(43)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (54)..(55)

<223> a, t, c, g, other or unknown

<400> 4

ccaagattgg aaagatctac cacagcnnsa ctnnkggagg tnsaccvvs gagnnkgatat  
60  
tcaacgtact ctcc  
74

<210> 5  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<220>  
<221> modified\_base  
<222> (20)..(21)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (26)..(27)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (53)..(54)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (59)..(60)  
<223> a, t, c, g, other or unknown

<400> 5  
tctggagagc acccagacmn ngtcsnngtg tcccttcttg tcctcgtcgt asnngcamnn  
60  
gtatccgatg atgtagtt  
78

<210> 6  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 6  
cttcgactgg tcccagtacc atggtaaatt gtggga  
36

<210> 7  
<211> 37  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

caccagtaag gaccatgctt ctggagagca cccagac

37

<210> 8

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligodeoxynucleotide

<400> 8

agatctttcc aatcttggag tcaccaactg ggtaggcggt accttc

46

<210> 9

<211> 793

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP22 nucleic acid sequence

<220>

<221> sig\_peptide

<222> (22)..(84)

<220>

<221> mat\_peptide

<222> (85)..(783)

<223> fusion protein of bilin-binding protein, Strep-Tag II  
and albumin-binding domain

<220>

<221> CDS

<222> (85)..(606)

<223> mature bilin-binding protein

<220>

<221> CDS

<222> (607)..(636)

<223> Strep-Tag II affinity tag

<220>

<221> CDS

<222> (637)..(783)

<223> albumin binding domain from Protein G

<400> 9

tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg  
51

Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
-20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac  
99

Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp  
-10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag  
147

Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln  
10 15 20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag  
195

Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu  
25 30 35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt  
243

Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser  
40 45 50

gtc aaa gtt tgc aac tac cac gta atc cac ggc aag gaa tac ttt att  
291

Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile  
55 60 65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac  
339

Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr  
70 75 80 85

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta  
387

His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val  
90 95 100

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac  
435

Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr  
105 110 115

gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga  
483

Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg  
120 125 130

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt  
531

Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu  
135 140 145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc  
579

Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
150 155 160 165

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag  
627

Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln  
170 175 180

ttc gaa aaa cca gct agc ctg gct gaa gct aaa gtt ctg gct aac cgt  
675

Phe Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg  
185 190 195

gaa ctg gac aaa tac ggt gtt tcc gac tac tac aaa aac ctc atc aac  
723

Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn  
200 205 210

aac gct aaa acc gtt gaa ggt gtt aaa gct ctg atc gac gaa att ctc  
771

Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu  
215 220 225

gca gca ctg ccg taataagctt  
793

Ala Ala Leu Pro  
230

<210> 10

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligodeoxynucleotide

<400> 10

gacggtgcct gtcccga

17

<210> 11

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligodeoxynucleotide

<400> 11

gactactggg gagccga

17

<210> 12  
<211> 522  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DigA nucleic  
acid sequence

<220>  
<221> CDS  
<222> (1)..(522)  
<223> mutein DigA without fusion parts

<400> 12  
gac gtg tac cac gac ggt gcc tgt ccc gaa gtc aag cca gtc gac aac  
48  
Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
1 5 10 15  
  
ttc gac tgg tcc cag tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac  
96  
Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr  
20 25 30  
  
ccc cat cac gag cgg aag tac gga aag tgc gga tgg gct gag tac act  
144  
Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
35 40 45  
  
cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc  
192  
Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly  
50 55 60  
  
aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag  
240  
Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
65 70 75 80  
  
att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag  
288  
Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu  
85 90 95  
  
ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga  
336  
Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
100 105 110  
  
tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc  
384  
Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val  
115 120 125

tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct  
432

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala  
130 135 140

gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg  
480

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu  
145 150 155 160

gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat  
522

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn  
165 170

<210> 13

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified\_base

<222> (29)..(30)

<223> a, t, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (38)..(39)

<223> a, t, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (47)..(48)

<223> a, t, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (50)..(51)

<223> a, t, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (53)..(54)

<223> a, t, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (56)..(57)

<223> a, t, c, g, t, other or unknown

<400> 13

ctggtcccag taccatggta aatggtggnn kgctgccnnk taccgccnnk nknnknnkaa

60

gtacggaaag tgcgga  
76

<210> 14  
<211> 1219  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fragment of  
pBBP24 nucleic acid sequence

<220>  
<221> sig\_peptide  
<222> (22)..(84)

<220>  
<221> mat\_peptide  
<222> (85)..(1209)  
<223> fusion protein of bilin-binding protein, Strep-Tag II  
and fragment of phage coat protein pIII, with  
interrupted reading frame

<220>  
<221> CDS  
<222> (85..207, 214..606)  
<223> mature bilin-binding protein with interrupted  
reading frame

<220>  
<221> CDS  
<222> (607)..(636)  
<223> Strep-Tag II affinity tag

<220>  
<221> misc\_feature  
<222> (637)..(639)  
<223> amber stop codon

<220>  
<221> CDS  
<222> (640)..(1209)  
<223> amino acids 217-406 of coat protein pIII

<400> 14  
tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg  
51

Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
-20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac  
99

Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp  
-10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag  
 147  
 Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln  
 10 15 20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag  
 195  
 Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu  
 25 30 35

aag tac gga aat taatga tgg gct gag tac act cct gaa ggc aag agt  
 243  
 Lys Tyr Gly Asn Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser  
 40 45 50

gtc aaa gtt tgc aac tac cac gta atc cac ggc aag gaa tac ttt att  
 291  
 Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile  
 55 60 65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac  
 339  
 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr  
 70 75 80

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta  
 387  
 His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val  
 85 90 95

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac  
 435  
 Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr  
 100 105 110 115

gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga  
 483  
 Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg  
 120 125 130

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt  
 531  
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu  
 135 140 145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc  
 579  
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
 150 155 160

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag  
 627  
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln  
 165 170 175

ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc  
 675

Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 180 185 190 195

tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct  
 723

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser  
 200 205 210

gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat  
 771

Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr  
 215 220 225

gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat  
 819

Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp  
 230 235 240

gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct  
 867

Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala  
 245 250 255

act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc  
 915

Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly  
 260 265 270 275

ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc  
 963

Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser  
 280 285 290

caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat  
 1011

Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn  
 295 300 305

ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct  
 1059

Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro  
 310 315 320

ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac  
 1107

Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp  
 325 330 335

aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc  
 1155

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala  
 340 345 350 355

acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag  
 1203

Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys  
 360 365 370

gag tct taataagctt  
1219  
Glu Ser

<210> 15  
<211> 522  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mutein DigA  
nucleic acid sequence

<220>  
<221> CDS  
<222> (1)..(522)  
<223> mutein DigA16 without fusion parts

<400> 15  
gac gtg tac cac gac ggt gcc tgt ccc gaa gtc aag cca gtc gac aac  
48  
Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
1 5 10 15  
ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg tac  
96  
Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr  
20 25 30  
ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac act  
144  
Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
35 40 45  
cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc  
192  
Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly  
50 55 60  
aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag  
240  
Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
65 70 75 80  
att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag  
288  
Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu  
85 90 95  
ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga  
336  
Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
100 105 110

tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc  
384

Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val  
115 120 125

tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct  
432

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala  
130 135 140

gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg  
480

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu  
145 150 155 160

gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat  
522

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn  
165 170

<210> 16

<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP21 nucleic acid sequence

<220>

<221> sig\_peptide

<222> (22)..(84)

<220>

<221> mat\_peptide

<222> (85)..(636)

<223> fusion protein of bilin-binding protein and Strep-Tag II

<220>

<221> sig\_peptide

<222> (658)..(717)

<220>

<221> mat\_peptide

<222> (718)..(1365)

<223> DsbC protein

<400> 16

tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg  
51

Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
-20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac  
99

Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp

	-10						-5						-1		1		5	
ggt 147	gcc	tgt	ccc	gaa	gtc	aag	cca	gtc	gac	aac	ttc	gac	tgg	tcc	cag			
Gly	Ala	Cys	Pro	Glu 10	Val	Lys	Pro	Val	Asp 15	Asn	Phe	Asp	Trp	Ser 20	Gln			
tac 195	cat	ggt	aaa	tgg	tgg	gaa	gtc	gcc	aaa	tac	ccc	aac	tca	gtt	gag			
Tyr	His	Gly	Lys 25	Trp	Trp	Glu	Val	Ala 30	Lys	Tyr	Pro	Asn	Ser 35	Val	Glu			
aag 243	tac	gga	aag	tgc	gga	tgg	gct	gag	tac	act	cct	gaa	ggc	aag	agt			
Lys	Tyr	Gly 40	Lys	Cys	Gly	Trp	Ala 45	Glu	Tyr	Thr	Pro	Glu 50	Gly	Lys	Ser			
gtc 291	aaa	gtt	tcg	aac	tac	cac	gta	atc	cac	ggc	aag	gaa	tac	ttt	att			
Val	Lys 55	Val	Ser	Asn	Tyr	His 60	Val	Ile	His	Gly	Lys 65	Glu	Tyr	Phe	Ile			
gaa 339	gga	act	gcc	tac	cca	gtt	ggt	gac	tcc	aag	att	gga	aag	atc	tac			
Glu 70	Gly	Thr	Ala	Tyr	Pro 75	Val	Gly	Asp	Ser	Lys 80	Ile	Gly	Lys	Ile	Tyr 85			
cac 387	agc	ctg	act	tac	gga	ggt	gtc	acc	aag	gag	aac	gta	ttc	aac	gta			
His	Ser	Leu	Thr	Tyr 90	Gly	Gly	Val	Thr	Lys 95	Glu	Asn	Val	Phe	Asn 100	Val			
ctc 435	tcc	act	gac	aac	aag	aac	tac	atc	atc	gga	tac	tac	tgc	aaa	tac			
Leu	Ser	Thr	Asp 105	Asn	Lys	Asn	Tyr	Ile 110	Ile	Gly	Tyr	Tyr	Cys 115	Lys	Tyr			
gac 483	gag	gac	aag	aag	gga	cac	caa	gac	ttc	gtc	tgg	gtg	ctc	tcc	aga			
Asp	Glu	Asp 120	Lys	Lys	Gly	His	Gln 125	Asp	Phe	Val	Trp	Val 130	Leu	Ser	Arg			
agc 531	atg	gtc	ctt	act	ggt	gaa	gcc	aag	acc	gct	gtc	gag	aac	tac	ctt			
Ser	Met 135	Val	Leu	Thr	Gly	Glu 140	Ala	Lys	Thr	Ala	Val 145	Glu	Asn	Tyr	Leu			
atc 579	ggc	tcc	cca	gta	gtc	gac	tcc	cag	aaa	ctg	gta	tac	agt	gac	ttc			
Ile 150	Gly	Ser	Pro	Val	Val 155	Asp	Ser	Gln	Lys	Leu 160	Val	Tyr	Ser	Asp	Phe 165			
tct 627	gaa	gcc	gcc	tgc	aag	gtc	aac	aat	agc	aac	tgg	tct	cac	ccg	cag			
Ser	Glu	Ala	Ala	Cys 170	Lys	Val	Asn	Asn	Ser 175	Asn	Trp	Ser	His	Pro 180	Gln			

ttc gaa aaa taataagctt cgggaagatt t atg aag aaa ggt ttt atg ttg  
678

Phe Glu Lys Met Lys Lys Gly Phe Met Leu  
-20 -15

ttt act ttg tta gcg gcg ttt tca ggc ttt gct cag gct gat gac gcg  
726

Phe Thr Leu Leu Ala Ala Phe Ser Gly Phe Ala Gln Ala Asp Asp Ala  
-10 -5 -1 1

gca att caa caa acg tta gcc aaa atg ggc atc aaa agc agc gat att  
774

Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser Ser Asp Ile  
5 10 15

cag ccc gcg cct gta gct ggc atg aag aca gtt ctg act aac agc ggc  
822

Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu Thr Asn Ser Gly  
20 25 30 35

gtg ttg tac atc acc gat gat ggt aaa cat atc att cag ggg cca atg  
870

Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile Ile Gln Gly Pro Met  
40 45 50

tat gac gtt agt ggc acg gct ccg gtc aat gtc acc aat aag atg ctg  
918

Tyr Asp Val Ser Gly Thr Ala Pro Val Asn Val Thr Asn Lys Met Leu  
55 60 65

tta aag cag ttg aat gcg ctt gaa aaa gag atg atc gtt tat aaa gcg  
966

Leu Lys Gln Leu Asn Ala Leu Glu Lys Glu Met Ile Val Tyr Lys Ala  
70 75 80

ccg cag gaa aaa cac gtc atc acc gtg ttt act gat att acc tgt ggt  
1014

Pro Gln Glu Lys His Val Ile Thr Val Phe Thr Asp Ile Thr Cys Gly  
85 90 95

tac tgc cac aaa ctg cat gag caa atg gca gac tac aac gcg ctg ggg  
1062

Tyr Cys His Lys Leu His Glu Gln Met Ala Asp Tyr Asn Ala Leu Gly  
100 105 110 115

atc acc gtg cgt tat ctt gct ttc ccg cgc cag ggg ctg gac agc gat  
1110

Ile Thr Val Arg Tyr Leu Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp  
120 125 130

gca gag aaa gaa atg aaa gct atc tgg tgt gcg aaa gat aaa aac aaa  
1158

Ala Glu Lys Glu Met Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys  
135 140 145

gcg ttt gat gat gtg atg gca ggt aaa agc gtc gca cca gcc agt tgc  
1206

Ala Phe Asp Asp Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys  
 150 155 160

gac gtg gat att gcc gac cat tac gca ctt ggc gtc cag ctt ggc gtt  
 1254

Asp Val Asp Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val  
 165 170 175

agc ggt act ccg gca gtt gtg ctg agc aat ggc aca ctt gtt ccg ggt  
 1302

Ser Gly Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu Val Pro Gly  
 180 185 190 195

tac cag ccg ccg aaa gag atg aaa gaa ttc ctc gac gaa cac caa aaa  
 1350

Tyr Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys  
 200 205 210

atg acc agc ggt aaa taattcgcgt agctt  
 1380

Met Thr Ser Gly Lys  
 215

<210> 17

<211> 2009

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
 pBBP27 nucleic acid sequence

<220>

<221> sig\_peptide

<222> (23)..(85)

<220>

<221> mat\_peptide

<222> (86)..(1999)

<223> fusion protein of alkaline phosphatase, linker peptide  
 Pro-Pro-Ser-Ala, mutein DigA16 and Strep-Tag II

<220>

<221> CDS

<222> (86)..(1435)

<223> mature part of alkaline phosphatase

<220>

<221> CDS

<222> (1436)..(1447)

<223> linker peptide Pro-Pro-Ser-Ala

<220>

<221> CDS

<222> (1448)..(1969)

<223> mutein DigA16

<220>

<221> CDS

<222> (1970)..(1999)

<223> Strep-Tag II affinity tag

<400> 17

tctagaacat ggagaaaata aa gtg aaa caa agc act att gca ctg gca ctc  
52

Val Lys Gln Ser Thr Ile Ala Leu Ala Leu  
-20 -15

tta ccg tta ctg ttt acc cct gtg aca aaa gcc cgg aca cca gaa atg  
100

Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr Pro Glu Met  
-10 -5 -1 1 5

cct gtt ctg gaa aac cgg gct gct cag ggc gat att act gca ccc ggc  
148

Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly  
10 15 20

ggt gct cgc cgt tta acg ggt gat cag act gcc gct ctg cgt gat tct  
196

Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser  
25 30 35

ctt agc gat aaa cct gca aaa aat att att ttg ctg att ggc gat ggg  
244

Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly  
40 45 50

atg ggg gac tcg gaa att act gcc gca cgt aat tat gcc gaa ggt gcg  
292

Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala  
55 60 65

ggc ggc ttt ttt aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac  
340

Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr  
70 75 80 85

act cac tat gcg ctg aat aaa aaa acc ggc aaa ccg gac tac gtc acc  
388

Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr  
90 95 100

gac tcg gct gca tca gca acc gcc tgg tca acc ggt gtc aaa acc tat  
436

Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr  
105 110 115

aac ggc gcg ctg ggc gtc gat att cac gaa aaa gat cac cca acg att  
484

Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile  
120 125 130

ctg gaa atg gca aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc  
 532  
 Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr  
 135 140 145

gca gag ttg cag gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc  
 580  
 Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr  
 150 155 160 165

tcg cgc aaa tgc tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt  
 628  
 Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly  
 170 175 180

aac gct ctg gaa aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt  
 676  
 Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu  
 185 190 195

aac gct cgt gcc gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct  
 724  
 Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala  
 200 205 210

gaa acg gca acc gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag  
 772  
 Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln  
 215 220 225

gca cag gcg cgt ggt tat cag ttg gtg agc gat gct gcc tca ctg aat  
 820  
 Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn  
 230 235 240 245

tcg gtg acg gaa gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct  
 868  
 Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala  
 250 255 260

gac ggc aat atg cca gtg cgc tgg cta gga ccg aaa gca acg tac cat  
 916  
 Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His  
 265 270 275

ggc aat atc gat aag ccc gca gtc acc tgt acg cca aat ccg caa cgt  
 964  
 Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg  
 280 285 290

aat gac agt gta cca acc ctg gcg cag atg acc gac aaa gcc att gaa  
 1012  
 Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu  
 295 300 305

ttg ttg agt aaa aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg  
 1060

Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala  
 310 315 320 325

tca atc gat aaa cag gat cat gct gcg aat cct tgt ggg caa att ggc  
 1108

Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly  
 330 335 340

gag acg gtc gat ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct  
 1156

Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala  
 345 350 355

aaa aag gag ggt aac acg ctg gtc ata gtc acc gct gat cac gcc cac  
 1204

Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His  
 360 365 370

gcc agc cag att gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag  
 1252

Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln  
 375 380 385

gcg cta aat acc aaa gat ggc gca gtg atg gtg atg agt tac ggg aac  
 1300

Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn  
 390 395 400 405

tcc gaa gag gat tca caa gaa cat acc ggc agt cag ttg cgt att gcg  
 1348

Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala  
 410 415 420

gcg tat ggc ccg cat gcc gcc aat gtt gtt gga ctg acc gac cag acc  
 1396

Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr  
 425 430 435

gat ctc ttc tac acc atg aaa gcc gct ctg ggg ctg aaa ccg cct agc  
 1444

Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser  
 440 445 450

gct gac gtg tac cac gac ggt gcc tgt ccc gaa gtc aag cca gtc gac  
 1492

Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp  
 455 460 465

aac ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg  
 1540

Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala  
 470 475 480 485

tac ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac  
 1588

Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr  
 490 495 500

act cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac  
1636

Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His  
505 510 515

ggc aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc  
1684

Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser  
520 525 530

aag att gga aag atc tac cac agc tac act att gga ggt gtg acc cag  
1732

Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln  
535 540 545

gag ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc  
1780

Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile  
550 555 560 565

gga tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg  
1828

Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu  
570 575 580

gtc tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc  
1876

Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr  
585 590 595

gct gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa  
1924

Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys  
600 605 610

ctg gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat agc  
1972

Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser  
615 620 625

aac tgg tct cac ccg cag ttc gaa aaa taataagctt  
2009

Asn Trp Ser His Pro Gln Phe Glu Lys  
630 635

<210> 18

<211> 2005

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP29 nucleic acid sequence

<220>

<221> sig\_peptide  
 <222> (22)..(84)  
 <220>  
 <221> mat\_peptide  
 <222> (85)..(1998)  
 <223> fusion protein of mutein DigA16, Strep-Tag II, linker  
 peptide Gly(5) and alkaline phosphatase

<220>  
 <221> CDS  
 <222> (85)..(606)  
 <223> mutein DigA16

<220>  
 <221> CDS  
 <222> (607)..(636)  
 <223> Strep-Tag II affinity tag

<220>  
 <221> CDS  
 <222> (637)..(651)  
 <223> linker peptide Gly-Gly-Gly-Gly-Gly

<220>  
 <221> CDS  
 <222> (652)..(1998)  
 <223> alkaline phosphatase without signalling sequence and  
 N-terminal Arg

<400> 18  
 tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg  
 51

Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
 -20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac  
 99

Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp  
 -10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag  
 147

Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln  
 10 15 20

tac cat ggt aaa tgg tgg cag gtc gcc gcg tac ccc gat cat att acg  
 195

Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr Pro Asp His Ile Thr  
 25 30 35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt  
 243

Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser  
 40 45 50

gtc aaa gtt tgc cgc tac tct gta atc cac ggc aag gaa tac ttt tcc  
 291  
 Val Lys Val Ser Arg Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser  
 55 60 65

gaa ggt acc gcc tac cca gtt ggt gac tcc aag att gga aag atc tac  
 339  
 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr  
 70 75 80 85

cac agc tac act att gga ggt gtg acc cag gag ggt gta ttc aac gta  
 387  
 His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val  
 90 95 100

ctc tcc act gac aac aag aac tac atc atc gga tac ttt tgc tgc tac  
 435  
 Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr  
 105 110 115

gac gag gac aag aag gga cac atg gac ttg gtc tgg gtg ctc tcc aga  
 483  
 Asp Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg  
 120 125 130

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt  
 531  
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu  
 135 140 145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc  
 579  
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
 150 155 160 165

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag  
 627  
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln  
 170 175 180

ttc gaa aaa ggt ggc ggc ggt ggt aca cca gaa atg cct gtt ctg gaa  
 675  
 Phe Glu Lys Gly Gly Gly Gly Gly Thr Pro Glu Met Pro Val Leu Glu  
 185 190 195

aac cgg gct gct cag ggc gat att act gca ccc ggc ggt gct cgc cgt  
 723  
 Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg  
 200 205 210

tta acg ggt gat cag act gcc gct ctg cgt gat tct ctt agc gat aaa  
 771  
 Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys  
 215 220 225

cct gca aaa aat att att ttg ctg att ggc gat ggg atg ggg gac tgc  
 819

Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser  
 230 235 240 245  
  
 gaa att act gcc gca cgt aat tat gcc gaa ggt gcg ggc ggc ttt ttt  
 867  
 Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe  
 250 255 260  
  
 aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac act cac tat gcg  
 915  
 Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala  
 265 270 275  
  
 ctg aat aaa aaa acc ggc aaa ccg gac tac gtc acc gac tcg gct gca  
 963  
 Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala  
 280 285 290  
  
 tca gca acc gcc tgg tca acc ggt gtc aaa acc tat aac ggc gcg ctg  
 1011  
 Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu  
 295 300 305  
  
 ggc gtc gat att cac gaa aaa gat cac cca acg att ctg gaa atg gca  
 1059  
 Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala  
 310 315 320 325  
  
 aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc gca gag ttg cag  
 1107  
 Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln  
 330 335 340  
  
 gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc tcg cgc aaa tgc  
 1155  
 Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys  
 345 350 355  
  
 tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt aac gct ctg gaa  
 1203  
 Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu  
 360 365 370  
  
 aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt aac gct cgt gcc  
 1251  
 Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala  
 375 380 385  
  
 gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct gaa acg gca acc  
 1299  
 Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr  
 390 395 400 405  
  
 gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag gca cag gcg cgt  
 1347  
 Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg  
 410 415 420

ggt tat cag ttg gtg agc gat gct gcc tca ctg aat tcg gtg acg gaa  
1395

Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu  
425 430 435

gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct gac ggc aat atg  
1443

Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met  
440 445 450

cca gtg cgc tgg cta gga ccg aaa gca acg tac cat ggc aat atc gat  
1491

Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp  
455 460 465

aag ccc gca gtc acc tgt acg cca aat ccg caa cgt aat gac agt gta  
1539

Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val  
470 475 480 485

cca acc ctg gcg cag atg acc gac aaa gcc att gaa ttg ttg agt aaa  
1587

Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys  
490 495 500

aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg tca atc gat aaa  
1635

Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys  
505 510 515

cag gat cat gct gcg aat cct tgt ggg caa att ggc gag acg gtc gat  
1683

Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp  
520 525 530

ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct aaa aag gag ggt  
1731

Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly  
535 540 545

aac acg ctg gtc ata gtc acc gct gat cac gcc cac gcc agc cag att  
1779

Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile  
550 555 560 565

gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag gcg cta aat acc  
1827

Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr  
570 575 580

aaa gat ggc gca gtg atg gtg atg agt tac ggg aac tcc gaa gag gat  
1875

Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp  
585 590 595

tca caa gaa cat acc ggc agt cag ttg cgt att gcg gcg tat ggc ccg  
1923

Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro  
600 605 610

cat gcc gcc aat gtt gtt gga ctg acc gac cag acc gat ctc ttc tac  
1971

His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr  
615 620 625

acc atg aaa gcc gct ctg ggg ctg aaa taagctt  
2005

Thr Met Lys Ala Ala Leu Gly Leu Lys  
630 635

<210> 19

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pBBP20  
amino acid sequence

<400> 19

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
-20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
-5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly  
30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr  
45 50 55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro  
60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly  
80 85 90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys  
95 100 105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly  
110 115 120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly  
125 130 135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val

140		145		150		155
Asp Ser Gln Lys	Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys					
	160		165			170
Val Asn Asn Ser	Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly					
	175		180			185
Gly Gly Ser Gly	Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser					
	190		195			200
Glu Gly Gly Gly	Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly					
	205		210			215
Gly Gly Ser Gly	Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala					
	220		225			230
Asn Lys Gly Ala	Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser					
	240		245			250
Asp Ala Lys Gly	Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala					
	255		260			265
Ile Asp Gly Phe	Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly					
	270		275			280
Ala Thr Gly Asp	Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly					
	285		290			295
Asp Gly Asp Asn	Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro					
	300		305			310
Ser Leu Pro Gln	Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly					
	320		325			330
Lys Pro Tyr Glu	Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg					
	335		340			345
Gly Val Phe Ala	Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe					
	350		355			360
Ser Thr Phe Ala	Asn Ile Leu Arg Asn Lys Glu Ser					
	365		370			375

<210> 20

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP22 amino acid sequence

<400> 20

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
-20 -15 -10

Thr	Val	Ala	Gln	Ala	Asp	Val	Tyr	His	Asp	Gly	Ala	Cys	Pro	Glu	Val	-5	-1	1	5	10
Lys	Pro	Val	Asp	Asn	Phe	Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	15			20	25
Glu	Val	Ala	Lys	Tyr	Pro	Asn	Ser	Val	Glu	Lys	Tyr	Gly	Lys	Cys	Gly	30			35	40
Trp	Ala	Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Asn	Tyr	45			50	55
His	Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ile	Glu	Gly	Thr	Ala	Tyr	Pro	60		65	70	75
Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Leu	Thr	Tyr	Gly		80		85	90
Gly	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys		95		100	105
Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	Asp	Glu	Asp	Lys	Lys	Gly	110		115		120
His	Gln	Asp	Phe	Val	Trp	Val	Leu	Ser	Arg	Ser	Met	Val	Leu	Thr	Gly	125		130		135
Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	Pro	Val	Val	140		145		150
Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	Ala	Ala	Cys	Lys		160		165	170
Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Pro	Ala	Ser		175		180	185
Leu	Ala	Glu	Ala	Lys	Val	Leu	Ala	Asn	Arg	Glu	Leu	Asp	Lys	Tyr	Gly	190		195		200
Val	Ser	Asp	Tyr	Tyr	Lys	Asn	Leu	Ile	Asn	Asn	Ala	Lys	Thr	Val	Glu	205		210		215
Gly	Val	Lys	Ala	Leu	Ile	Asp	Glu	Ile	Leu	Ala	Ala	Leu	Pro			220		225		230

<210> 21

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DigA amino acid sequence

<400> 21

Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
 1 5 10 15  
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr  
 20 25 30  
 Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
 35 40 45  
 Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly  
 50 55 60  
 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
 65 70 75 80  
 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu  
 85 90 95  
 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
 100 105 110  
 Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val  
 115 120 125  
 Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala  
 130 135 140  
 Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu  
 145 150 155 160  
 Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn  
 165 170

<210> 22

<211> 394

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP24 amino acid sequence

<400> 22

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
 -20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
 -5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
 15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Asn Trp Ala  
 30 35 40

Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val

45					50					55					
Ile	His	Gly	Lys	Glu	Tyr	Phe	Ile	Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly
60					65					70					75
Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Leu	Thr	Tyr	Gly	Gly	Val
				80					85					90	
Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys	Asn	Tyr
			95					100					105		
Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	Asp	Glu	Asp	Lys	Lys	Gly	His	Gln
		110					115					120			
Asp	Phe	Val	Trp	Val	Leu	Ser	Arg	Ser	Met	Val	Leu	Thr	Gly	Glu	Ala
	125					130					135				
Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	Pro	Val	Val	Asp	Ser
140					145					150					155
Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	Ala	Ala	Cys	Lys	Val	Asn
				160					165					170	
Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Lys	Ala	Gly	Gly	Gly
			175					180					185		
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly
		190					195					200			
Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	205					210					215				
Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys
220					225					230					235
Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala
				240					245					250	
Lys	Gly	Lys	Leu	Asp	Ser	Val	Ala	Thr	Asp	Tyr	Gly	Ala	Ala	Ile	Asp
			255					260					265		
Gly	Phe	Ile	Gly	Asp	Val	Ser	Gly	Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr
		270					275					280			
Gly	Asp	Phe	Ala	Gly	Ser	Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly
	285					290					295				
Asp	Asn	Ser	Pro	Leu	Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu
300					305					310					315
Pro	Gln	Ser	Val	Glu	Cys	Arg	Pro	Phe	Val	Phe	Gly	Ala	Gly	Lys	Pro
				320					325					330	
Tyr	Glu	Phe	Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	Gly	Val
			335					340					345		
Phe	Ala	Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	Phe	Ser	Thr

350	355	360
Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser		
365	370	

<210> 23  
 <211> 174  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Mutein DigA16  
 amino acid sequence

<400> 23  
 Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
 1 5 10 15  
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr  
 20 25 30  
 Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
 35 40 45  
 Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly  
 50 55 60  
 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
 65 70 75 80  
 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu  
 85 90 95  
 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
 100 105 110  
 Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val  
 115 120 125  
 Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala  
 130 135 140  
 Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu  
 145 150 155 160  
 Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn  
 165 170

<210> 24  
 <211> 205  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fragment of

pBBP21 amino acid sequence

<400> 24

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
-20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
-5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly  
30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr  
45 50 55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro  
60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly  
80 85 90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys  
95 100 105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly  
110 115 120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly  
125 130 135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val  
140 145 150 155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys  
160 165 170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys  
175 180

<210> 25

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP21 amino acid sequence

<400> 25

Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly  
-20 -15 -10 -5

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met



Ala	Ala	Gln	Gly	Asp	Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	Arg	Leu	Thr	15	20	25
Gly	Asp	Gln	Thr	Ala	Ala	Leu	Arg	Asp	Ser	Leu	Ser	Asp	Lys	Pro	Ala	30	35	40
Lys	Asn	Ile	Ile	Leu	Leu	Ile	Gly	Asp	Gly	Met	Gly	Asp	Ser	Glu	Ile	45	50	55
Thr	Ala	Ala	Arg	Asn	Tyr	Ala	Glu	Gly	Ala	Gly	Gly	Phe	Phe	Lys	Gly	60	65	70
Ile	Asp	Ala	Leu	Pro	Leu	Thr	Gly	Gln	Tyr	Thr	His	Tyr	Ala	Leu	Asn	80	85	90
Lys	Lys	Thr	Gly	Lys	Pro	Asp	Tyr	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	95	100	105
Thr	Ala	Trp	Ser	Thr	Gly	Val	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	110	115	120
Asp	Ile	His	Glu	Lys	Asp	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	Lys	Ala	125	130	135
Ala	Gly	Leu	Ala	Thr	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	140	145	150
Thr	Pro	Ala	Ala	Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	160	165	170
Pro	Ser	Ala	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	175	180	185
Gly	Lys	Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	190	195	200
Thr	Leu	Gly	Gly	Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	205	210	215
Glu	Trp	Gln	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	220	225	230
Gln	Leu	Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	Asn	240	245	250
Gln	Gln	Lys	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	Met	Pro	Val	255	260	265
Arg	Trp	Leu	Gly	Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	Ile	Asp	Lys	Pro	270	275	280
Ala	Val	Thr	Cys	Thr	Pro	Asn	Pro	Gln	Arg	Asn	Asp	Ser	Val	Pro	Thr	285	290	295
Leu	Ala	Gln	Met	Thr	Asp	Lys	Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	300	305	310

Lys	Gly	Phe	Phe	Leu	Gln	Val	Glu	Gly	Ala	Ser	Ile	Asp	Lys	Gln	Asp	320	325	330
His	Ala	Ala	Asn	Pro	Cys	Gly	Gln	Ile	Gly	Glu	Thr	Val	Asp	Leu	Asp	335	340	345
Glu	Ala	Val	Gln	Arg	Ala	Leu	Glu	Phe	Ala	Lys	Lys	Glu	Gly	Asn	Thr	350	355	360
Leu	Val	Ile	Val	Thr	Ala	Asp	His	Ala	His	Ala	Ser	Gln	Ile	Val	Ala	365	370	375
Pro	Asp	Thr	Lys	Ala	Pro	Gly	Leu	Thr	Gln	Ala	Leu	Asn	Thr	Lys	Asp	380	385	390
Gly	Ala	Val	Met	Val	Met	Ser	Tyr	Gly	Asn	Ser	Glu	Glu	Asp	Ser	Gln	400	405	410
Glu	His	Thr	Gly	Ser	Gln	Leu	Arg	Ile	Ala	Ala	Tyr	Gly	Pro	His	Ala	415	420	425
Ala	Asn	Val	Val	Gly	Leu	Thr	Asp	Gln	Thr	Asp	Leu	Phe	Tyr	Thr	Met	430	435	440
Lys	Ala	Ala	Leu	Gly	Leu	Lys	Pro	Pro	Ser	Ala	Asp	Val	Tyr	His	Asp	445	450	455
Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	Asp	Trp	Ser	Gln	460	465	470
Tyr	His	Gly	Lys	Trp	Trp	Gln	Val	Ala	Ala	Tyr	Pro	Asp	His	Ile	Thr	480	485	490
Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	495	500	505
Val	Lys	Val	Ser	Arg	Tyr	Ser	Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ser	510	515	520
Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	525	530	535
His	Ser	Tyr	Thr	Ile	Gly	Gly	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val	540	545	550
Leu	Ser	Thr	Asp	Asn	Lys	Asn	Tyr	Ile	Ile	Gly	Tyr	Phe	Cys	Ser	Tyr	560	565	570
Asp	Glu	Asp	Lys	Lys	Gly	His	Met	Asp	Leu	Val	Trp	Val	Leu	Ser	Arg	575	580	585
Ser	Met	Val	Leu	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	590	595	600
Ile	Gly	Ser	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	605	610	615

Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln  
620 625 630 635

Phe Glu Lys

<210> 27

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
pBBP29 amino acid sequence

<400> 27

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
-20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
-5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
15 20 25

Gln Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly  
30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr  
45 50 55

Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro  
60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly  
80 85 90

Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys  
95 100 105

Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly  
110 115 120

His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly  
125 130 135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val  
140 145 150 155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys  
160 165 170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly  
175 180 185

Gly Gly Thr Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly

190					195					200					
Asp	Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	Arg	Leu	Thr	Gly	Asp	Gln	Thr
205						210					215				
Ala	Ala	Leu	Arg	Asp	Ser	Leu	Ser	Asp	Lys	Pro	Ala	Lys	Asn	Ile	Ile
220					225					230					235
Leu	Leu	Ile	Gly	Asp	Gly	Met	Gly	Asp	Ser	Glu	Ile	Thr	Ala	Ala	Arg
				240					245					250	
Asn	Tyr	Ala	Glu	Gly	Ala	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	Ala	Leu
			255					260					265		
Pro	Leu	Thr	Gly	Gln	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	Thr	Gly
		270					275					280			
Lys	Pro	Asp	Tyr	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	Trp	Ser
	285					290					295				
Thr	Gly	Val	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	His	Glu
300					305					310					315
Lys	Asp	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	Lys	Ala	Ala	Gly	Leu	Ala
				320					325					330	
Thr	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	Thr	Pro	Ala	Ala
			335					340					345		
Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	Pro	Ser	Ala	Thr
		350					355					360			
Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	Gly	Lys	Gly	Ser
	365					370					375				
Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	Thr	Leu	Gly	Gly
380					385					390					395
Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	Glu	Trp	Gln	Gly
				400					405					410	
Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	Gln	Leu	Val	Ser
			415					420					425		
Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	Asn	Gln	Gln	Lys	Pro
		430					435					440			
Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	Met	Pro	Val	Arg	Trp	Leu	Gly
	445					450					455				
Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	Ile	Asp	Lys	Pro	Ala	Val	Thr	Cys
460					465					470					475
Thr	Pro	Asn	Pro	Gln	Arg	Asn	Asp	Ser	Val	Pro	Thr	Leu	Ala	Gln	Met
				480					485					490	
Thr	Asp	Lys	Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	Lys	Gly	Phe	Phe

495					500					505					
Leu	Gln	Val	Glu	Gly	Ala	Ser	Ile	Asp	Lys	Gln	Asp	His	Ala	Ala	Asn
	510						515					520			
Pro	Cys	Gly	Gln	Ile	Gly	Glu	Thr	Val	Asp	Leu	Asp	Glu	Ala	Val	Gln
	525					530					535				
Arg	Ala	Leu	Glu	Phe	Ala	Lys	Lys	Glu	Gly	Asn	Thr	Leu	Val	Ile	Val
540						545					550				555
Thr	Ala	Asp	His	Ala	His	Ala	Ser	Gln	Ile	Val	Ala	Pro	Asp	Thr	Lys
				560					565					570	
Ala	Pro	Gly	Leu	Thr	Gln	Ala	Leu	Asn	Thr	Lys	Asp	Gly	Ala	Val	Met
			575					580					585		
Val	Met	Ser	Tyr	Gly	Asn	Ser	Glu	Glu	Asp	Ser	Gln	Glu	His	Thr	Gly
	590						595					600			
Ser	Gln	Leu	Arg	Ile	Ala	Ala	Tyr	Gly	Pro	His	Ala	Ala	Asn	Val	Val
	605						610					615			
Gly	Leu	Thr	Asp	Gln	Thr	Asp	Leu	Phe	Tyr	Thr	Met	Lys	Ala	Ala	Leu
620						625					630				635
Gly Leu Lys															

<210> 28

<211> 174

<212> PRT

<213> wild type sequence of mature bilin binding protein of *Pieris brassicae*

<400> 28

Asp	Val	Tyr	His	Asp	Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp
				5					10					15
Asn	Phe	Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala
				20					25					30
Lys	Tyr	Pro	Asn	Ser	Val	Glu	Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala
				35					40					45
Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Asn	Tyr	His
				50					55					60
Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ile	Glu	Gly	Thr	Ala	Tyr	Pro
				65					70					75
Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Leu	Thr	Tyr
				80					85					90
Gly	Gly	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp
				95					100					105
Asn	Lys	Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	Asp	Glu	Asp
				110					115					120
Lys	Lys	Gly	His	Gln	Asp	Phe	Val	Trp	Val	Leu	Ser	Arg	Ser	Met
				125					130					135
Val	Leu	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile
				140					145					150
Gly	Ser	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe
				155					160					165

Ser Glu Ala Ala Cys Lys Val Asn Asn  
170